SEQUENCE LISTING

<110> Duvick, Jonathan P.
       Gilliam, Jacob T.
       Maddox, Joyce R.

<120> Amino Polyol Amine Oxidase
       Polynucleotides and Related Polypeptides and Methods of Use

<130> 1184C

<140> 09/771,045
<141> 2001-01-26

<150> US 60/092,936
<151> 1998-07-15

<150> US 60/135,391
<151> 1999-05-21

<150> US 09/352,159
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gcttggactg ttgggaccac ttccgtcccg ggtctccgac catgaaacag gtaatggacc     120
attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatggggtca cagctcgatt     180
ggaggacgcc cgagaagcct tgttcgcgcc accacggctt gtcccatacg aagactatct     240
tgctatagta gcccaggata gaattttccg ccaatgcttg cttctcggcg ggaagaggtg     300
gtgaaaatgt caaggtggga tacaaggttg tcggtaacga aaccancacc tttttgcttc     360
ggaacacggc gc                                                         372

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tacaaggttg tcggtaacga aaccaccacc tttttgcttc ggaacacggc gcccgaggcc     120
gatcgtactg tacagccgga tgccgactgc tcaatttcag cgacggggt gttgaggtgc     180
ac                                                                    182

<210> 3
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
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<400> 3
tggtttcgtt accgacaacc ttgtatccc                                    29

<210> 4
<211> 28
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<223> Designed oligonucleotide for 5' RACE, 21968


<400> 4
gagttggtcc cagacagact tttgtcgt                                     28

<210> 5
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Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
 1               5                  10                  15

gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt      96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
            20                  25                  30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt     144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
        35                  40                  45

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac     192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
    50                  55                  60

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag     240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65                  70                  75                  80

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac     288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
                85                  90                  95

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag     336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
            100                 105                 110

gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc     384
```

```
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
    115                 120                 125

gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg        432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
    130                 135                 140

ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg        480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
145                 150                 155                 160

cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt        528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
                165                 170                 175

gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag        576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
                180                 185                 190

agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg        624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
                195                 200                 205

cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg        672
Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
    210                 215                 220

tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct        720
Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
225                 230                 235                 240

gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc        768
Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
                245                 250                 255

gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg        816
Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
                260                 265                 270

tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca        864
Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
                275                 280                 285

ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta        912
Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
                290                 295                 300

tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa        960
Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
305                 310                 315                 320

tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc       1008
Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
                325                 330                 335

gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg       1056
Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
                340                 345                 350

aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac       1104
Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
                355                 360                 365
```

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caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg          1152
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
    370             375             380

gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga          1200
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
385             390             395             400

gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg          1248
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
            405             410             415

gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg          1296
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
            420             425             430

tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa          1344
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
            435             440             445

cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca               1386
Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
    450             455             460

tag                                                                       1389
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<210> 6
<211> 462
<212> PRT
<213> Exophiala spinifera

<400> 6

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  1             5              10             15
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            20             25             30
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
        35             40             45
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
    50             55             60
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65             70             75             80
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
            85             90             95
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
            100            105            110
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
        115            120            125
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
    130            135            140
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
145            150            155            160
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
            165            170            175
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
        180            185            190
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
        195            200            205
Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
    210            215            220
Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
```

```
     225                      230                      235                      240
Glu  Ile  Glu  Gln  Ser  Ala  Ser  Gly  Cys  Thr  Val  Arg  Ser  Ala  Ser  Gly
                    245                      250                      255
Ala  Val  Phe  Arg  Ser  Lys  Lys  Val  Val  Val  Ser  Leu  Pro  Thr  Thr  Leu
               260                      265                      270
Tyr  Pro  Thr  Leu  Thr  Phe  Ser  Pro  Pro  Leu  Pro  Ala  Glu  Lys  Gln  Ala
          275                      280                      285
Leu  Ala  Glu  Asn  Ser  Ile  Leu  Gly  Tyr  Tyr  Ser  Lys  Ile  Val  Phe  Val
     290                      295                      300
Trp  Asp  Lys  Pro  Trp  Trp  Arg  Glu  Gln  Gly  Phe  Ser  Gly  Val  Leu  Gln
305                      310                      315                      320
Ser  Ser  Cys  Asp  Pro  Ile  Ser  Phe  Ala  Arg  Asp  Thr  Ser  Ile  Asp  Val
                    325                      330                      335
Asp  Arg  Gln  Trp  Ser  Ile  Thr  Cys  Phe  Met  Val  Gly  Asp  Pro  Gly  Arg
               340                      345                      350
Lys  Trp  Ser  Gln  Gln  Ser  Lys  Gln  Val  Arg  Gln  Lys  Ser  Val  Trp  Asp
          355                      360                      365
Gln  Leu  Arg  Ala  Ala  Tyr  Glu  Asn  Ala  Gly  Ala  Gln  Val  Pro  Glu  Pro
     370                      375                      380
Ala  Asn  Val  Leu  Glu  Ile  Glu  Trp  Ser  Lys  Gln  Gln  Tyr  Phe  Gln  Gly
385                      390                      395                      400
Ala  Pro  Ser  Ala  Val  Tyr  Gly  Leu  Asn  Asp  Leu  Ile  Thr  Leu  Gly  Ser
                    405                      410                      415
Ala  Leu  Arg  Thr  Pro  Phe  Lys  Ser  Val  His  Phe  Val  Gly  Thr  Glu  Thr
               420                      425                      430
Ser  Leu  Val  Trp  Lys  Gly  Tyr  Met  Glu  Gly  Ala  Ile  Arg  Ser  Gly  Gln
          435                      440                      445
Arg  Gly  Ala  Ala  Glu  Val  Val  Ala  Ser  Leu  Val  Pro  Ala  Ala
     450                      455                      460
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<213> Exophiala spinifera

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Asp  Asn  Val  Ala  Asp  Val  Val  Val  Val  Gly  Ala  Gly  Leu  Ser  Gly  Leu
 1                  5                      10                      15

gag  acg  gca  cgc  aaa  gtc  cag  gcc  gcc  ggt  ctg  tcc  tgc  ctc  gtt  ctt        96
Glu  Thr  Ala  Arg  Lys  Val  Gln  Ala  Ala  Gly  Leu  Ser  Cys  Leu  Val  Leu
               20                      25                      30

gag  gcg  atg  gat  cgt  gta  ggg  gga  aag  act  ctg  agc  gta  caa  tcg  ggt       144
Glu  Ala  Met  Asp  Arg  Val  Gly  Gly  Lys  Thr  Leu  Ser  Val  Gln  Ser  Gly
          35                      40                      45

ccc  ggc  agg  acg  act  atc  aac  gac  ctc  ggc  gct  gcg  tgg  atc  aat  gac       192
Pro  Gly  Arg  Thr  Thr  Ile  Asn  Asp  Leu  Gly  Ala  Ala  Trp  Ile  Asn  Asp
     50                      55                      60
```

```
agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag      240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65                  70                  75                  80

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac      288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
                     85                  90                  95

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag      336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
                100                 105                 110

gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc      384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
            115                 120                 125

gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg      432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
        130                 135                 140

ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg      480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
145                 150                 155                 160

cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt      528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
                165                 170                 175

gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag      576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
                180                 185                 190

agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg      624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
                195                 200                 205

cag tat gtg cga tgc aaa aca g gtgcgtgtgg tgtcgtctca ggtgggggac       676
Gln Tyr Val Arg Cys Lys Thr
        210                 215

tcgtttctca gtggtcattc cag gt atg cag tcg att tgc cat gcc atg tca     728
                           Gly Met Gln Ser Ile Cys His Ala Met Ser
                                           220                 225

aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa      776
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu
                230                 235                 240

att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc      824
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala
                245                 250                 255

gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat      872
Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr
            260                 265                 270

ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg      920
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu
        275                 280                 285

gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg      968
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp
```

| 290 | | | | 295 | | | | 300 | | | | 305 | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|

```
290                        295                        300                        305
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg        1016
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser
            310                       315               320

agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat        1064
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp
            325               330               335

cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag        1112
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys
        340               345               350

tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa        1160
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln
        355               360               365

ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc        1208
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala
370               375               380               385

aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct        1256
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala
                390               395               400

ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg        1304
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala
            405               410               415

ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct        1352
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser
        420               425               430

tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga        1400
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg
        435               440               445

ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag              1442
Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
450               455               460
```

<210> 8
<211> 462
<212> PRT
<213> Exophiala spinifera

<400> 8
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Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
 1               5                   10                  15
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
            20                  25                  30
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
            35                  40                  45
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
    50                  55                  60
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65                  70                  75                  80
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
            85                  90                  95
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
```

```
              100                     105                     110
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
          115                     120                     125
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
      130                     135                     140
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
145                     150                     155                     160
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
              165                     170                     175
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
          180                     185                     190
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
          195                     200                     205
Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
      210                     215                     220
Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
225                     230                     235                     240
Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
              245                     250                     255
Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
          260                     265                     270
Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
      275                     280                     285
Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
      290                     295                     300
Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
305                     310                     315                     320
Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
              325                     330                     335
Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
          340                     345                     350
Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
          355                     360                     365
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
      370                     375                     380
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
385                     390                     395                     400
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
              405                     410                     415
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
          420                     425                     430
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
          435                     440                     445
Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
      450                     455                     460
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<210> 9
<211> 458
<212> PRT
<213> Exophiala spinifera

<400> 9
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              20                      25                      30
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
          35                      40                      45
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
      50                      55                      60
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65                      70                      75                      80
```

```
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
                85                  90                  95
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
                100                 105                 110
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
                115                 120                 125
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
    130                 135                 140
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
145                 150                 155                 160
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
                165                 170                 175
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
                180                 185                 190
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
                195                 200                 205
Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly
    210                 215                 220
Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met
225                 230                 235                 240
Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro
                245                 250                 255
Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro
                260                 265                 270
Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln
                275                 280                 285
Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Pro Arg Ser Lys
    290                 295                 300
His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr
305                 310                 315                 320
Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn
                325                 330                 335
Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser
                340                 345                 350
Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly
    355                 360                 365
Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr
    370                 375                 380
Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg
385                 390                 395                 400
Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu
                405                 410                 415
Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg
                420                 425                 430
Ser Glu Arg Arg Ser Arg Val Phe Ile Ser Leu Glu Arg Arg Arg Leu
    435                 440                 445
Phe Gly Lys Gly Ile Trp Lys Gly Pro Tyr
    450                 455
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<210> 10
<211> 1392
<212> DNA
<213> Exophiala spinifera

<220>
<221> CDS
<222> (1)...(1389)

<221> misc_feature
<222> (1)...(3)
<223> Extra lysine in K:trAPAO
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<400> 10
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt        48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1               5                   10                  15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt        96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
            20                  25                  30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg       144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
            35                  40                  45

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat       192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
        50                  55                  60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg       240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65                  70                  75                  80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa       288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
                85                  90                  95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag       336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
            100                 105                 110

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg       384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
            115                 120                 125

atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag       432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
        130                 135                 140

cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac       480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145                 150                 155                 160

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc       528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
                165                 170                 175

ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc       576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
            180                 185                 190

aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc       624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
            195                 200                 205

ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc       672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
        210                 215                 220

atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc       720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225                 230                 235                 240

gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg       768
```

```
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
                245                 250                 255

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc    816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
            260                 265                 270

ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa    864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
            275                 280                 285

gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc    912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
    290                 295                 300

gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc    960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305                 310                 315                 320

caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac   1008
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
                325                 330                 335

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga   1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
                340                 345                 350

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg   1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
            355                 360                 365

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag   1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
    370                 375                 380

ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa   1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385                 390                 395                 400

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt   1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
                405                 410                 415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag   1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
            420                 425                 430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt   1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
            435                 440                 445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca        1389
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
    450                 455                 460

tag                                                                1392
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<210> 11
<211> 463
<212> PRT
<213> Exophiala spinifera

<400> 11

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Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly
1               5                   10                  15
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
            20              25                  30
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
        35              40                  45
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
    50              55                  60
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65              70                  75                      80
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
                85                  90                  95
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
            100             105                 110
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
        115                 120                 125
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
    130             135                 140
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145             150                 155                     160
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
            165                 170                 175
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
            180                 185                 190
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
    195                 200                 205
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
    210                 215                 220
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225             230                 235                     240
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
                245                 250                 255
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
            260                 265                 270
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
    275                 280                 285
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
    290                 295                 300
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305             310                 315                     320
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
            325                 330                 335
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
            340                 345                 350
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
    355                 360                 365
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
    370                 375                 380
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385                 390                 395                 400
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
            405                 410                 415
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
            420                 425                 430
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
        435                 440                 445
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
    450                 455                 460
```

<210> 12
<211> 34

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<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence designed for cloning DNA into
      expression vectors, N23256


<400> 12
ggggaattca aagacaacgt tgcggacgtg gtag                              34

<210> 13
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence designed for cloning DNA into
      expression vectors, N23259


<400> 13
ggggcggccg cctatgctgc tggcaccagg ctag                             34

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide for 3' RACE, N21965

<400> 14
tggtttcgtt accgacaacc ttgtatccc                                   29

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide for 5' race, N21968

<400> 15
gagttggtcc cagacagact tttgtcgt                                    28

<210> 16
<211> 1673
<212> DNA
<213> Exophiala spinifera

<220>
<221> sig_peptide
<222> (1)...(267)
<223> yeast alpha mating factor secretion signal.

<221> CDS
<222> (1)...(1662)

<400> 16
atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc   48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
```

```
                      -85                      -80                       -75

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa          96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            -70                  -65                      -60

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc        144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        -55                  -50                      -45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg        192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    -40                  -35                      -30

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta        240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
-25                  -20                      -15                  -10

tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg        288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
                -5                   1                   5

gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc        336
Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg
            10                   15                  20

aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat        384
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp
        25                   30                  35

cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg        432
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr
40                   45                  50                      55

act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc        480
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser
                60                   65                  70

gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag        528
Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln
            75                   80                  85

agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act        576
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr
        90                   95                  100

aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca        624
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala
    105                  110                 115

ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc        672
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser
120                  125                 130                 135

ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg        720
Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val
                140                 145                 150

agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc        768
Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu
            155                 160                 165
```

```
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac        816
Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His
        170             175             180

gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt        864
Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly
185             190             195

ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga        912
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg
200             205             210             215

tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt        960
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu
            220             225             230

gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag       1008
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln
            235             240             245

tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga       1056
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg
            250             255             260

agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg       1104
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu
        265             270             275

aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat       1152
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn
280             285             290             295

tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg       1200
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro
            300             305             310

tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac       1248
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp
            315             320             325

ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg       1296
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp
            330             335             340

tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa       1344
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln
        345             350             355

cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca       1392
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala
360             365             370             375

gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc       1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu
            380             385             390

gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc       1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala
            395             400             405

gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg       1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
```

```
                410                      415                      420
ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg        1584
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
    425                 430                 435

aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca        1632
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
440                 445                 450                 455

gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c                   1673
Glu Val Val Ala Ser Leu Val Pro Ala Ala
                460                 465
```


<210> 17
<211> 554
<212> PRT
<213> Exophiala spinifera

<220>
<221> SIGNAL
<222> (1)...(89)

<400> 17

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Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
              -85                 -80                 -75
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
          -70                 -65                 -60
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
          -55                 -50                 -45
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
          -40                 -35                 -30
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
-25                 -20                 -15                 -10
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
              -5                  1                   5
Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg
          10                  15                  20
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp
    25                  30                  35
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr
40                  45                  50                  55
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser
              60                  65                  70
Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln
          75                  80                  85
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr
          90                  95                  100
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala
    105                 110                 115
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser
120                 125                 130                 135
Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val
              140                 145                 150
Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu
          155                 160                 165
Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His
          170                 175                 180
Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly
          185                 190                 195
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg
```

```
200                    205                    210                    215
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu
            220                    225                    230
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln
            235                    240                    245
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg
            250                    255                    260
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu
            265                    270                    275
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn
280                    285                    290                    295
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro
            300                    305                    310
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp
            315                    320                    325
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp
            330                    335                    340
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln
            345                    350                    355
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala
360                    365                    370                    375
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu
            380                    385                    390
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala
            395                    400                    405
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
            410                    415                    420
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
            425                    430                    435
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
440                    445                    450                    455
Glu Val Val Ala Ser Leu Val Pro Ala Ala
            460                    465
```

<210> 18
<211> 2079
<212> DNA
<213> Unknown

<220>
<223> GST:K:trAPAO 2079 nt. Translation starting at nt 1
      - 687, gst fusion + polylinker, 688-2076,
      K:trAPAO, extra lysine underlined; 2077-2079, stop
      codon. For bacterial expression.


<221> CDS
<222> (1)...(2076)

<221> misc_feature
<222> (1)...(687)
<223> gst fusion + polylinker

<221> misc_feature
<222> (688)...(2076)
<223> K:trAPAO

<221> misc_feature
<222> (688)...(690)
<223> Extra lysine

<400> 18

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atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc        48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1               5              10                  15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg        96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
            20              25                  30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg       144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35              40                  45

ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa       192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50              55                  60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac       240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65              70                  75                  80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa       288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85                  90                  95

gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt       336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100             105                 110

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa       384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
        115                 120                 125

atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat       432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130                 135                 140

ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat       480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145                 150                 155                 160

gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta       528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165                 170                 175

gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac       576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180                 185                 190

ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc       624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
            195                 200                 205

acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt       672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
    210                 215                 220

gga tcc ccg gaa ttc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc       720
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly
225                 230                 235                 240

gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt       768
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly
```

```
                       245                     250                     255

ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act       816
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr
            260                     265                     270

ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc       864
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly
            275                     280                     285

gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt       912
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe
            290                     295                     300

gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca       960
Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser
305                     310                     315                     320

atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac      1008
Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp
                325                     330                     335

tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc      1056
Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro
            340                     345                     350

gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg      1104
Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala
            355                     360                     365

agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt      1152
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys
            370                     375                     380

gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc      1200
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile
385                     390                     395                     400

aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt      1248
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe
                405                     410                     415

ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg      1296
Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser
                420                     425                     430

gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag      1344
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln
                435                     440                     445

tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac      1392
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His
            450                     455                     460

ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca      1440
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr
465                     470                     475                     480

gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt      1488
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val
            485                     490                     495
```

```
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt      1536
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu
        500             505             510

ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat      1584
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr
        515             520             525

agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc      1632
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
        530             535             540

ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga      1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
545             550             555             560

gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg      1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
            565             570             575

gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga      1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
        580             585             590

caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg      1824
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
        595             600             605

gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag      1872
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
        610             615             620

cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat      1920
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
625             630             635             640

ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat      1968
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
            645             650             655

ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg      2016
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
            660             665             670

gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg      2064
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
        675             680             685

gtg cca gca gca tag                                                   2079
Val Pro Ala Ala
        690
```

<210> 19
<211> 692
<212> PRT
<213> Unknown

<220>
<223> GST:K:trAPAO, for bacterial expression

<400> 19

```
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1                   5                   10                  15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
        20                  25                  30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35                  40                  45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50                  55                  60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65                  70                  75                  80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85                  90                  95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100                 105                 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
        115                 120                 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130                 135                 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145                 150                 155                 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165                 170                 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180                 185                 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
        195                 200                 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
    210                 215                 220
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly
225                 230                 235                 240
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly
            245                 250                 255
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr
            260                 265                 270
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly
        275                 280                 285
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe
    290                 295                 300
Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser
305                 310                 315                 320
Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp
            325                 330                 335
Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro
        340                 345                 350
Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala
    355                 360                 365
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys
370                 375                 380
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile
385                 390                 395                 400
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe
            405                 410                 415
Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser
        420                 425                 430
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln
        435                 440                 445
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His
    450                 455                 460
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr
465                 470                 475                 480
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val
            485                 490                 495
```

```
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu
            500             505             510
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr
            515             520             525
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
        530             535             540
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
545             550             555             560
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
            565             570             575
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
            580             585             590
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
        595             600             605
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
    610             615             620
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
625             630             635             640
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
            645             650             655
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
            660             665             670
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
        675             680             685
Val Pro Ala Ala
        690
```

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<210> 20
<211> 1464
<212> DNA

<213> Unknown

<220>
<223> Nucleotide sequence of K:trAPAO translational
      fusion with barley alpha amylase signal sequence,
      for expression and secretion of the mature trAPAO
      in maize. Nucleotides 1-72, barley alpha amylase
      signal sequence, nucleotides 73-75, added lysine
      residue; nucleotides 76 -1464 , trAPAO cDNA.


<221> sig_peptide
<222> (1)...(72)
<223> Barley alpha amylase signal sequence

<221> misc_feature
<222> (73)...(1464)
<223> K:trAPAOcDNA

<221> CDS
<222> (1)...(1461)

<221> misc_feature
<222> (73)...(75)
<223> Added lysine residue

<400> 20
atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc      48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
            -20             -15             -10
```

```
ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta        96
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
            -5                  1               5

gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag       144
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
        10                  15              20

gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg       192
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
25                  30                  35                  40

gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac       240
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
                    45                  50                  55

gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc       288
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
                60                  65                  70

aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act       336
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
            75                  80                  85

gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct       384
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
        90                  95                  100

tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa       432
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
105                 110                 115                 120

ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac       480
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp
                125                 130                 135

ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg       528
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala
                140                 145                 150

cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca       576
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala
            155                 160                 165

aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc       624
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
        170                 175                 180

atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat       672
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
185                 190                 195                 200

att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca       720
Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr
                205                 210                 215

ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc       768
Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
                220                 225                 230

tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc       816
Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
```

|       | 235 |     |     |     |     | 240 |     |     |     |     | 245 |     |     |     |     |      |
|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|

```
                235                           240                           245

    ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag      864
    Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys
        250                 255                 260

    gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca      912
    Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser
    265                 270                 275                 280

    cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg      960
    Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu
                        285                 290                 295

    ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc     1008
    Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg
                        300                 305                 310

    gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca     1056
    Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser
                315                 320                 325

    ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc     1104
    Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr
                330                 335                 340

    tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag     1152
    Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys
    345                 350                 355                 360

    cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag     1200
    Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu
                        365                 370                 375

    aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag     1248
    Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu
                        380                 385                 390

    tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg     1296
    Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly
                        395                 400                 405

    ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag     1344
    Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys
                410                 415                 420

    agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat     1392
    Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr
    425                 430                 435                 440

    atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg     1440
    Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val
                        445                 450                 455

    gct agc ctg gtg cca gca gca tag                                     1464
    Ala Ser Leu Val Pro Ala Ala
                460
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<210> 21
<211> 487
<212> PRT

<213> Unknown

<220>
<221> SIGNAL
<222> (1)...(24)

<223> K:trAPAO translational fusion with barley alpha
      amylase signal sequence, for expression and
      secretion of the mature trAPAO in maize.

<400> 21
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
                -20              -15                   -10
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
            -5               1               5
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
    10              15              20
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
25              30              35                      40
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
            45              50              55
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
        60              65                  70
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
    75              80              85
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
    90              95              100
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
105             110             115                     120
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp
            125             130             135
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala
            140             145             150
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala
        155             160             165
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
    170             175             180
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
185             190             195                     200
Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr
            205             210             215
Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
        220             225             230
Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
        235             240             245
Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys
    250             255             260
Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser
265             270             275                     280
Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu
            285             290             295
Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg
            300             305             310
Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser
            315             320             325
Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr
            330             335             340
Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys
345             350             355                     360
Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu
            365             370             375
Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu

```
          380                          385                          390
Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly
          395                          400                          405
Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys
          410                          415                          420
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr
425                          430                          435                          440
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val
                    445                          450                          455
Ala Ser Leu Val Pro Ala Ala
                    460
```

<210> 22
<211> 1803
<212> DNA
<213> Exophiala spinifera

<220>
<221> CDS
<222> (1)...(1800)

<400> 22
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atg gca ctt gca ccg agc tac atc aat ccc cca aac gtc gcc tcc cca      48
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1               5                   10                  15

gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg      96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
                20                  25                  30

aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct     144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
            35                  40                  45

gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc     192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
        50                  55                  60

ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac     240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65                  70                  75                  80

tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg     288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
                85                  90                  95

ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg     336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
                100                 105                 110

cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc     384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
            115                 120                 125

acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg     432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
        130                 135                 140

gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc     480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145                 150                 155                 160
```

```
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta        528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
            165             170                 175

ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc        576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
            180                 185                 190

aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta        624
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
            195                 200                 205

tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg        672
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
            210                 215                 220

act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct        720
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225                     230                 235                 240

cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg        768
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
                245                 250                 255

gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa        816
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
                260                 265                 270

gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc        864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
            275                 280                 285

gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta        912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
            290                 295                 300

gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc        960
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305                     310                 315                 320

agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt       1008
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
                325                 330                 335

aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa       1056
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
                340                 345                 350

aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca       1104
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
            355                 360                 365

ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca       1152
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
            370                 375                 380

tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa       1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385                     390                 395                 400

aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt       1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
```

```
                        405                    410                    415
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc        1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
            420                    425                    430

ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg        1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
            435                    440                    445

cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc        1392
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
            450                    455                    460

tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att        1440
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
465                    470                    475                    480

acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc        1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
                    485                    490                    495

aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac        1536
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
                500                    505                    510

gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc        1584
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
            515                    520                    525

gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat        1632
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
            530                    535                    540

ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc        1680
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545                    550                    555                    560

aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg        1728
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
                    565                    570                    575

tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt        1776
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
                580                    585                    590

gtg gct agc ctg gtg cca gca gca tag                                    1803
Val Ala Ser Leu Val Pro Ala Ala
            595                    600
```

<210> 23
<211> 600
<212> PRT
<213> Exophiala spinifera

<400> 23

```
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1               5                   10                  15
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
            20                  25                  30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
```

```
                35                        40                        45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
    50                        55                        60
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65                        70                        75                        80
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
                85                        90                        95
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
                100                       105                       110
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
                115                       120                       125
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
    130                       135                       140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145                       150                       155                       160
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
                165                       170                       175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
                180                       185                       190
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
                195                       200                       205
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
    210                       215                       220
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225                       230                       235                       240
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
                245                       250                       255
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
                260                       265                       270
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
                275                       280                       285
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
    290                       295                       300
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305                       310                       315                       320
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
                325                       330                       335
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
                340                       345                       350
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
    355                       360                       365
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
370                       375                       380
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385                       390                       395                       400
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
                405                       410                       415
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
                420                       425                       430
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
    435                       440                       445
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
    450                       455                       460
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
465                       470                       475                       480
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
                485                       490                       495
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
                500                       505                       510
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
    515                       520                       525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
```

```
         530                      535                      540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545                      550                      555                      560
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
                565                      570                      575
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
                580                      585                      590
Val Ala Ser Leu Val Pro Ala Ala
            595                      600
```

<210> 24
<211> 3003
<212> DNA
<213> Unknown

<220>
<223> Sequence is barley alpha amylase signal sequence:
        esp1 mat: an artificial spacer sequence and
        K:trAPAO


<221> sig_peptide
<222> (1)...(72)
<223> Barley alpha amylase signal sequence

<221> misc_feature
<222> (73)...(1575)
<223> esp1 mat

<221> misc_feature
<222> (1576)...(1611)
<223> spacer sequence

<221> misc_feature
<222> (1612)...(3000)
<223> K:trAPAO

<221> CDS
<222> (1)...(3000)

<221> misc_feature
<222> (1612)...(1614)
<223> Extra lysine

<400> 24
```
atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc     48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
                -20                 -15                 -10


ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct     96
Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala
                -5                   1                   5


ggg atg gtg gtc ggc acg act act act gtc ccc ggc acc act gcg acc    144
Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
     10                  15                  20


gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt    192
Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
  25                  30                  35                  40


gcg cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act    240
```

```
Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr
                45              50              55
```

```
gca tat ggt cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc        288
Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu
            60              65              70
```

```
cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt        336
Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly
        75              80              85
```

```
gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag        384
Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu
        90              95              100
```

```
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa        432
Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu
105             110             115             120
```

```
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc        480
Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala
                125             130             135
```

```
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg        528
Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu
            140             145             150
```

```
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg        576
Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly
        155             160             165
```

```
ttc cta gac caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca        624
Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala
        170             175             180
```

```
gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg        672
Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala
185             190             195             200
```

```
ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca        720
Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro
                205             210             215
```

```
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc        768
Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe
                220             225             230
```

```
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc        816
Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu
        235             240             245
```

```
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat        864
Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp
    250             255             260
```

```
ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag        912
Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu
265             270             275             280
```

```
tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc        960
Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg
                285             290             295
```

```
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc    1008
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala
            300             305             310

aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat    1056
Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr
            315             320             325

ctc gag gag gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt    1104
Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu
    330             335             340

gga gca tat ccc att gga tcc cca ggg atc gga tcg cct caa gat cag    1152
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln
345             350             355             360

att gcc gcc att gag acc gag gta aga ttc cag tgt cct tct gcc atc    1200
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile
                365             370             375

gtg gct cag gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac    1248
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr
            380             385             390

tac aat gcg acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg    1296
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val
            395             400             405

tac cac agc tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca    1344
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala
    410             415             420

agt gcg acc gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc    1392
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala
425             430             435             440

tgg gcg gcc ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa    1440
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln
            445             450             455

gtg ccg aat gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt    1488
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val
            460             465             470

gac gtc tct cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt    1536
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg
            475             480             485

tat tat act gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc    1584
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly
    490             495             500

agc ggc gga ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg    1632
Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val
505             510             515             520

gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc    1680
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
            525             530             535

cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta    1728
```

```
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
            540                 545                 550

ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc      1776
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
            555                 560                 565

aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta      1824
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
            570                 575                 580

tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg      1872
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
585                 590                 595                 600

act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct      1920
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
                    605                 610                 615

cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg      1968
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
                    620                 625                 630

gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa      2016
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
            635                 640                 645

gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc      2064
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
            650                 655                 660

gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta      2112
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
665                 670                 675                 680

gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc      2160
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
                    685                 690                 695

agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt      2208
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
            700                 705                 710

aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa      2256
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
            715                 720                 725

aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca      2304
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
730                 735                 740

ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca      2352
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
745                 750                 755                 760

tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa      2400
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
                    765                 770                 775

aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt      2448
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
                    780                 785                 790
```

tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc    2496
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
        795              800              805

ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg    2544
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
        810              815              820

cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc    2592
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
825              830              835              840

tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att    2640
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
            845              850              855

acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc    2688
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
            860              865              870

aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac    2736
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
        875              880              885

gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc    2784
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
    890              895              900

gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat    2832
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
905              910              915              920

ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc    2880
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
            925              930              935

aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg    2928
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
            940              945              950

tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt    2976
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
        955              960              965

gtg gct agc ctg gtg cca gca gca tag                                 3003
Val Ala Ser Leu Val Pro Ala Ala
        970              975


<210> 25
<211> 1000
<212> PRT
<213> Unknown

<220>
<221> SIGNAL
<222> (1)...(24)

<223> Barley alpha amylase signal sequence: espl mat: an
      artifical spacer and k:trAPAO

```
<400> 25
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
              -20                 -15                    -10
Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala
              -5                  1                   5
Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
    10                  15                  20
Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
25                  30                  35                      40
Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr
              45                  50                      55
Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu
          60                  65                  70
Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly
        75                  80                  85
Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu
    90                  95                  100
Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu
105                 110                 115                     120
Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala
              125                 130                 135
Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu
              140                 145                 150
Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly
          155                 160                 165
Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala
    170                 175                 180
Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala
185                 190                 195                     200
Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro
              205                 210                 215
Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe
              220                 225                 230
Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu
          235                 240                 245
Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp
    250                 255                 260
Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu
265                 270                 275                     280
Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg
              285                 290                 295
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala
          300                 305                 310
Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr
    315                 320                 325
Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu
    330                 335                 340
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln
345                 350                 355                     360
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile
              365                 370                 375
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr
          380                 385                 390
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val
    395                 400                 405
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala
    410                 415                 420
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala
425                 430                 435                     440
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln
              445                 450                     455
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val
```

```
                    460                          465                          470
    Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg
            475                          480                          485
    Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly
            490                          495                          500
    Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val
    505                          510                          515                          520
    Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
                    525                          530                          535
    Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
                    540                          545                          550
    Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
            555                          560                          565
    Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
            570                          575                          580
    Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
    585                          590                          595                          600
    Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
                    605                          610                          615
    Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
                    620                          625                          630
    Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
            635                          640                          645
    Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
            650                          655                          660
    Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
    665                          670                          675                          680
    Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
                    685                          690                          695
    Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
                    700                          705                          710
    Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
            715                          720                          725
    Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
            730                          735                          740
    Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
    745                          750                          755                          760
    Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
                    765                          770                          775
    Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
                    780                          785                          790
    Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
            795                          800                          805
    Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
            810                          815                          820
    Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
    825                          830                          835                          840
    Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
                    845                          850                          855
    Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
                    860                          865                          870
    Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
            875                          880                          885
    Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
            890                          895                          900
    Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
    905                          910                          915                          920
    Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
                    925                          930                          935
    Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
            940                          945                          950
    Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
```

```
        955                   960                  965
Val Ala Ser Leu Val Pro Ala Ala
   970                   975


<210> 26
<211> 2976
<212> DNA
<213> Unknown

<220>
<223> Barley alpha amylase signal sequence: BEST1
      mature: artificial spacer: and K:trAPAO.  For
      plant expression.


<221> sig_peptide
<222> (1)...(72)
<223> Barley alpha amylase signal sequence

<221> mat_peptide
<222> (73)...(1545)
<223> BEST1 mature

<221> misc_feature
<222> (1546)...(1584)
<223> spacer sequence

<221> misc_feature
<222> (1585)...(2973)
<223> K:trAPAO

<221> CDS
<222> (1)...(2973)

<221> misc_feature
<222> (1585)...(1587)
<223> Extra lysine

<400> 26
atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc       48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
                -20                 -15                 -10

ctc tcc gcc tcc ctc gcc agc ggc acg gat ttt ccg gtc cgc agg acc       96
Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr
             -5                  1                   5

gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc      144
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg
        10                  15                  20

gga ata ccc tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg      192
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
   25                  30                  35                  40

ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt      240
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe
                45                  50                  55

ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc      288
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala
                60                  65                  70
```

```
ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca        336
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser
            75              80                  85

ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc        384
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly
        90              95                  100

ggc ttc gcc ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg        432
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala
105              110                 115                 120

ctt gcg cga cag ggc gtc gtc gtg gtg acg ttt aac tat cgg acg aac        480
Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn
                125                 130                 135

atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc        528
Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr
            140                 145                 150

gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg        576
Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg
            155                 160                 165

tgg gtg cag agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg        624
Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val
    170                 175                 180

acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc        672
Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu
185                 190                 195                 200

acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt        720
Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser
                205                 210                 215

cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg        768
Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser
                220                 225                 230

ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca        816
Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro
            235                 240                 245

gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac        864
Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp
        250                 255                 260

ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg        912
Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu
265                 270                 275                 280

ccg cag acc gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt        960
Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val
                285                 290                 295

cgg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg       1008
Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly
                300                 305                 310

cgc gcg ccg atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg       1056
```

```
Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala
        315             320             325

cag ttt ggc gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac    1104
Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp
    330             335             340

ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat    1152
Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn
345             350             355             360

cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag    1200
Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln
            365             370             375

ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga    1248
Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly
            380             385             390

aga gcg ccg gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg    1296
Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val
            395             400             405

ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc    1344
Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro
    410             415             420

acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc    1392
Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val
425             430             435             440

cgg ttc gcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct    1440
Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro
            445             450             455

gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc    1488
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg
            460             465             470

gcg gcg gtg gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc    1536
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly
            475             480             485

gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc    1584
Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
    490             495             500

aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt    1632
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
505             510             515             520

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt    1680
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
            525             530             535

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg    1728
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
            540             545             550

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat    1776
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
            555             560             565
```

```
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg      1824
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
    570             575             580

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa      1872
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
585             590             595             600

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag      1920
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
            605             610             615

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg      1968
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
            620             625             630

atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag      2016
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
            635             640             645

cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac      2064
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
    650             655             660

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc      2112
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
665             670             675             680

ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc      2160
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
                685             690             695

aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc      2208
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
            700             705             710

ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc      2256
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
        715             720             725

atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc      2304
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
    730             735             740

gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg      2352
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
745             750             755             760

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc      2400
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
            765             770             775

ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa      2448
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
            780             785             790

gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc      2496
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
        795             800             805

gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc      2544
```

```
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
    810             815             820

caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac    2592
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
825             830             835             840

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga    2640
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
            845             850             855

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg    2688
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
            860             865             870

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag    2736
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
        875             880             885

ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa    2784
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
    890             895             900

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt    2832
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
905             910             915             920

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag    2880
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
            925             930             935

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt    2928
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
            940             945             950

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca        2973
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
    955             960             965

tag                                                                2976

<210> 27
<211> 991
<212> PRT
<213> Unknown

<220>
<221> SIGNAL
<222> (1)...(24)

<223> Barley alpha amylase signal sequence: BEST1
      mature: artificial spacer: and K:trAPAO.  For
      plant expression.

<400> 27
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
                -20             -15             -10
Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr
                -5                  1               5
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg
    10              15              20
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
```

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25                      30                              35                        40
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe
                45                          50                        55
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala
                60                      65                        70
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser
            75                      80                        85
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly
        90                      95                        100
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala
105                     110                     115                       120
Leu Ala Arg Gln Gly Val Val Val Thr Phe Asn Tyr Arg Thr Asn
                125                         130                       135
Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr
                140                         145                       150
Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg
                155                         160                       165
Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val
        170                         175                       180
Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu
185                     190                     195                       200
Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser
                205                         210                       215
Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser
                220                         225                       230
Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro
                235                         240                       245
Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp
            250                         255                       260
Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu
265                     270                     275                       280
Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val
                285                         290                       295
Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly
                300                         305                       310
Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala
            315                         320                       325
Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp
            330                         335                       340
Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn
345                     350                         355                   360
Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln
                365                         370                       375
Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly
                380                         385                       390
Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val
                395                         400                       405
Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro
            410                         415                       420
Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val
425                     430                         435                   440
Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro
                445                         450                       455
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg
                460                         465                       470
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly
            475                         480                       485
Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
            490                         495                   500
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
505                     510                     515                       520
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
```

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                        525                 530                 535
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
            540                 545                 550
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
        555                 560                 565
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
    570                 575                 580
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
585                 590                 595                 600
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
                605                 610                 615
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
            620                 625                 630
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
        635                 640                 645
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
    650                 655                 660
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
665                 670                 675                 680
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
                685                 690                 695
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
            700                 705                 710
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
        715                 720                 725
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
        730                 735                 740
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
745                 750                 755                 760
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
                765                 770                 775
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
            780                 785                 790
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
        795                 800                 805
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
    810                 815                 820
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
825                 830                 835                 840
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
                845                 850                 855
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
            860                 865                 870
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
        875                 880                 885
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
    890                 895                 900
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
905                 910                 915                 920
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
            925                 930                 935
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
        940                 945                 950
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
    955                 960                 965
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<210> 28
<211> 3618
<212> DNA
<213> Unknown

<220>

<223> gst:esp1:sp:K:trAPAO, 3618. 1-687, gst +
      polylinker; 688-2190, esp1 mat; 2191-2226 spacer;
      2227-3615, K:trAPAO, 3616-3618, stop codon. For
      bacterial expression.


<221> CDS
<222> (1)...(3615)

<221> misc_feature
<222> (1)...(687)
<223> gst + polylinker

<221> mat_peptide
<222> (688)...(2190)
<223> esp1 mat

<221> misc_feature
<222> (2191)...(2226)
<223> spacer sequence

<221> misc_feature
<222> (2227)...(3615)
<223> K:trAPAO

<221> misc_feature
<222> (2227)...(2229)
<223> Extra lysine

<400> 28

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atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc      48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1           5                  10                  15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg      96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
            20                  25                  30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg     144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35                  40                  45

ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa     192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50                  55                  60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac     240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65                  70                  75                  80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa     288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85                  90                  95

gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt     336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100                 105                 110

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa     384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
        115                 120                 125
```

```
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat        432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130             135             140

ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat        480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145             150             155             160

gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta        528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165             170             175

gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac        576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180             185             190

ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc        624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
        195             200             205

acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt        672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
    210             215             220

gga tcc ccg gaa ttc gct cct act gtc aag att gat gct ggg atg gtg        720
Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val
225             230             235             240

gtc ggc acg act act act gtc ccc ggc acc act gcg acc gtc agc gag        768
Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu
                245             250             255

ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt gcg cct cct        816
Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro
            260             265             270

act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act gca tat ggt        864
Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly
    275             280             285

cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc cgt gag att        912
Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile
    290             295             300

acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt gaa agt gag        960
Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu
305             310             315             320

gac tgc ctg aac ctc aac atc tac gtc cca gga act gag aac aca aac       1008
Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn
            325             330             335

aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa tat ggt tgg       1056
Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp
        340             345             350

aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc aat cag gat       1104
Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp
        355             360             365

gtc atc gcc gtg acc atc aac tac aga acg aac att ctg ggg ttc cct       1152
Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro
```

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                370                        375                         380

gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg ttc cta gac        1200
Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp
385                     390                     395                 400

caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca gcc ttt ggc        1248
Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly
                    405                     410                 415

ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg ggg ggc aga        1296
Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg
                420                     425                 430

agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca ccc ttc cga        1344
Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg
                435                     440                 445

gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc ccc aag gga        1392
Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly
            450                     455                 460

gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc aac tgt acc        1440
Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr
465                     470                     475                 480

acc agt atc gac atc ttg agt tgt atg aga aga gtc gat ctc gcc act        1488
Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr
                    485                     490                 495

ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag tac acg ttg        1536
Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu
                500                     505                 510

gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc acg act ggt        1584
Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly
                515                     520                 525

gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc aac gac gga        1632
Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly
            530                     535                 540

ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat ctc gag gag        1680
Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu
545                     550                     555                 560

gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt gga gca tat        1728
Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr
                    565                     570                 575

ccc att gga tcc cca ggg atc gga tcg cct caa gat cag att gcc gcc        1776
Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala
                580                     585                 590

att gag acc gag gta aga ttc cag tgt cct tct gcc atc gtg gct cag        1824
Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln
                595                     600                 605

gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac tac aat gcg        1872
Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala
            610                     615                 620
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acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg tac cac agc      1920
Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser
625             630             635                 640

tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca agt gcg acc      1968
Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr
                645             650             655

gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc tgg gcg gcc      2016
Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala
            660             665             670

ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa gtg ccg aat      2064
Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn
            675             680             685

gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt gac gtc tct      2112
Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser
            690             695             700

cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt tat tat act      2160
Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr
705             710             715             720

gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc agc ggc gga      2208
Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly Ser Gly Gly
                725             730             735

ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg gta gtg gtg      2256
Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val
            740             745             750

ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc      2304
Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala
            755             760             765

ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag      2352
Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys
770             775             780

act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc      2400
Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu
785             790             795             800

ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg      2448
Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu
            805             810             815

ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat      2496
Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn
            820             825             830

tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt      2544
Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly
            835             840             845

gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc      2592
Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu
            850             855             860

ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag      2640
Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys
```

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865                    870                    875                    880
gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac       2688
Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr
                885                    890                    895

tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag       2736
Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln
                900                    905                    910

atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt       2784
Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu
                915                    920                    925

ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc       2832
Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe
        930                    935                    940

tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg       2880
Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met
945                    950                    955                    960

cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg       2928
Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val
                        965                    970                    975

cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt       2976
His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys
                980                    985                    990

aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg       3024
Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val
                995                    1000                   1005

gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct       3072
Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro
        1010                   1015                   1020

ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac       3120
Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr
1025                   1030                   1035                   1040

tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa       3168
Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln
                        1045                   1050                   1055

ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc       3216
Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala
                1060                   1065                   1070

aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc       3264
Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe
                1075                   1080                   1085

atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta       3312
Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val
        1090                   1095                   1100

cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc       3360
Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala
1105                   1110                   1115                   1120
```

```
ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg     3408
Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser
            1125            1130                1135

aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac     3456
Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn
            1140            1145                1150

gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt     3504
Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val
            1155            1160                1165

cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa     3552
His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu
            1170            1175                1180

ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc     3600
Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser
1185                1190            1195                1200

ctg gtg cca gca gca tag                                             3618
Leu Val Pro Ala Ala
                1205
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<210> 29
<211> 1205
<212> PRT
<213> Unknown

<220>
<223> Gst:esp1:sp:K:trAPAO.   For bacterial expression.

<400> 29
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1               5                   10                  15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
            20                  25                  30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35                  40                  45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50                  55                  60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65                  70                  75                  80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85                  90                  95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
                100                 105                 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
            115                 120                 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
            130                 135                 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145                 150                 155                 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165                 170                 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
                180                 185                 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
            195                 200                 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
            210                 215                 220
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50

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Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val
225                 230                 235                 240
Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu
            245                 250                 255
Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro
            260                 265                 270
Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly
        275                 280                 285
Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile
        290                 295                 300
Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu
305                 310                 315                 320
Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn
            325                 330                 335
Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp
            340                 345                 350
Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp
        355                 360                 365
Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro
        370                 375                 380
Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp
385                 390                 395                 400
Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly
            405                 410                 415
Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg
            420                 425                 430
Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg
        435                 440                 445
Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly
        450                 455                 460
Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr
465                 470                 475                 480
Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr
            485                 490                 495
Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu
            500                 505                 510
Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly
        515                 520                 525
Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly
        530                 535                 540
Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu
545                 550                 555                 560
Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr
            565                 570                 575
Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala
            580                 585                 590
Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln
        595                 600                 605
Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala
        610                 615                 620
Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser
625                 630                 635                 640
Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr
            645                 650                 655
Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala
            660                 665                 670
Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn
        675                 680                 685
Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser
        690                 695                 700
Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr
705                 710                 715                 720
```

```
Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly Ser Gly Gly
            725                 730                 735
Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val
            740                 745                 750
Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala
            755                 760                 765
Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys
770                 775                 780
Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu
785                 790                 795                 800
Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu
            805                 810                 815
Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn
            820                 825                 830
Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly
            835                 840                 845
Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu
    850                 855                 860
Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys
865                 870                 875                 880
Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr
            885                 890                 895
Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln
            900                 905                 910
Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu
            915                 920                 925
Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe
    930                 935                 940
Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met
945                 950                 955                 960
Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val
            965                 970                 975
His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys
            980                 985                 990
Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val
            995                 1000                1005
Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro
    1010                1015                1020
Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr
1025                1030                1035                1040
Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln
            1045                1050                1055
Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala
            1060                1065                1070
Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe
            1075                1080                1085
Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val
            1090                1095                1100
Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala
1105                1110                1115                1120
Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser
            1125                1130                1135
Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn
            1140                1145                1150
Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val
            1155                1160                1165
His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu
    1170                1175                1180
Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser
1185                1190                1195                1200
Leu Val Pro Ala Ala
            1205
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<210> 30
<211> 3591
<212> DNA
<213> Unknown

<220>
<223> Open reading frame of BEST1:K:trAPAO fusion for
      bacterial expression vector pGEX-4T-1 or similar
      vector. gst:BEST1:sp:K:trAPAO fusion, 3591 nt.
      1-687 gst
      + polylinker,  688-2163, BEST1 mature; 2164-2199,
      spacer, 2200-3588, K:trAPAO


<221> misc_feature
<222> (1)...(687)
<223> gst + polylinker

<221> mat_peptide
<222> (688)...(2163)
<223> BEST1 mature

<221> misc_feature
<222> (2164)...(2199)
<223> spacer sequence

<221> misc_feature
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<221> CDS
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<221> misc_feature
<222> (2200)...(2202)
<223> Extra lysine

<400> 30
atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc    48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1               5                   10                  15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg    96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
            20                  25                  30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg   144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35                  40                  45

ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa   192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
        50                  55                  60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac   240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65                  70                  75                  80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa   288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85                  90                  95
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gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt      336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100                 105                 110

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa      384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
            115                 120                 125

atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat      432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
        130                 135                 140

ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat      480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145                 150                 155                 160

gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta      528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165                 170                 175

gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac      576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180                 185                 190

ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc      624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
            195                 200                 205

acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt      672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
        210                 215                 220

gga tcc ccg gaa ttc acg gat ttt ccg gtc cgc agg acc gat ctg ggc      720
Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly
225                 230                 235                 240

cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc gga ata ccc      768
Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro
                245                 250                 255

tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg ccc caa cac      816
Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His
                260                 265                 270

gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt ggc tcc gac      864
Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp
                275                 280                 285

tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc ccc ggc gtg      912
Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val
        290                 295                 300

agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca ggc gct aaa      960
Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys
305                 310                 315                 320

ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc ggc ttc gcc     1008
Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala
                325                 330                 335

ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg ctt gcg cga     1056
```

```
      Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg
              340                 345                 350

      cag ggc gtc gtc gtg gtg acg ttt aac tat cgg acg aac atc ctg ggc    1104
      Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly
              355                 360                 365

      ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc gga act tcg    1152
      Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser
      370                 375                 380

      ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg tgg gtg cag    1200
      Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln
      385                 390                 395                 400

      agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg acg gtc ttt    1248
      Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe
                          405                 410                 415

      ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc acc tcg ccg    1296
      Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro
                          420                 425                 430

      ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt cca ggg ctg    1344
      Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu
                  435                 440                 445

      acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg ggc gag cgc    1392
      Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg
              450                 455                 460

      ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca gcc acc ctg    1440
      Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu
      465                 470                 475                 480

      atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac ctg cgc agg    1488
      Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg
                          485                 490                 495

      ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg ccg cag acc    1536
      Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr
                  500                 505                 510

      gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt cgg gtc ctg    1584
      Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu
                  515                 520                 525

      atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg cgc gcg ccg    1632
      Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly Arg Ala Pro
              530                 535                 540

      atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg cag ttt ggc    1680
      Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala Gln Phe Gly
      545                 550                 555                 560

      gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac ggc cgg gcc    1728
      Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp Gly Arg Ala
                          565                 570                 575

      acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat cag ttc aat    1776
      Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn
                  580                 585                 590
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cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag ggc gcg ccc      1824
Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro
        595             600             605

gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga aga gcg ccg      1872
Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly Arg Ala Pro
610             615             620

gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg ttc aag ctc      1920
Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu
625             630             635             640

gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc acg ccc gcc      1968
Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala
            645             650             655

gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc cgg ttc gcc      2016
Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala
            660             665             670

aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct gcc tat tct      2064
Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser
            675             680             685

acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc gcg gcg gtg      2112
Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val
        690             695             700

gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc gcc aag gcg      2160
Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala
705             710             715             720

ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc aaa gac aac      2208
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn
                725             730             735

gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg      2256
Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr
            740             745             750

gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg      2304
Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala
        755             760             765

atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc      2352
Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly
770             775             780

agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac      2400
Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn
785             790             795             800

caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag      2448
Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu
            805             810             815

ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt aca      2496
Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr
        820             825             830

acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca      2544
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```
Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala
        835             840             845

agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag    2592
Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu
        850             855             860

cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac    2640
His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp
865             870             875             880

agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct    2688
Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala
                885             890             895

gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa    2736
Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu
                900             905             910

gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc    2784
Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala
            915             920             925

acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat    2832
Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr
930             935             940

atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag    2880
Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys
945             950             955             960

gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att    2928
Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile
                965             970             975

gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg    2976
Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val
                980             985             990

ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc    3024
Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro
        995             1000            1005

acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg    3072
Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala
        1010            1015            1020

gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac    3120
Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp
1025            1030            1035            1040

aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc    3168
Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser
                1045            1050            1055

tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga    3216
Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg
                1060            1065            1070

caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg    3264
Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp
                1075            1080            1085
```

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tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc      3312
Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu
    1090                1095                1100

cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac      3360
Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn
1105                1110                1115                1120

gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg      3408
Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro
                1125                1130                1135

agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc      3456
Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu
                1140                1145                1150

aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta      3504
Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu
                1155                1160                1165

gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt      3552
Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly
    1170                1175                1180

gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag                  3591
Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
1185                1190                1195
```

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<210> 31
<211> 1196
<212> PRT
<213> Unknown

<220>
<223> BEST1:K:trAPAO fusion for bacterial expression
      vector pGEX-4T-1 or similar vector.

<400> 31
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1               5                   10                  15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
                20                  25                  30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35                  40                  45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
        50                  55                  60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65                  70                  75                  80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85                  90                  95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
                100                 105                 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
        115                 120                 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
        130                 135                 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145                 150                 155                 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165                 170                 175
```

```
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180                 185                 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
            195                 200                 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
    210                 215                 220
Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly
225                 230                 235                 240
Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro
            245                 250                 255
Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His
            260                 265                 270
Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp
            275                 280                 285
Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val
    290                 295                 300
Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys
305                 310                 315                 320
Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala
            325                 330                 335
Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg
            340                 345                 350
Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly
            355                 360                 365
Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser
    370                 375                 380
Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln
385                 390                 395                 400
Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe
            405                 410                 415
Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro
            420                 425                 430
Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu
            435                 440                 445
Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg
    450                 455                 460
Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu
465                 470                 475                 480
Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg
            485                 490                 495
Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr
            500                 505                 510
Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu
            515                 520                 525
Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly Arg Ala Pro
    530                 535                 540
Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala Gln Phe Gly
545                 550                 555                 560
Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp Gly Arg Ala
            565                 570                 575
Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn
            580                 585                 590
Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro
            595                 600                 605
Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly Arg Ala Pro
    610                 615                 620
Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu
625                 630                 635                 640
Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala
            645                 650                 655
Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala
            660                 665                 670
```

```
Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser
        675                 680                 685
Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val
        690             695             700
Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala
705             710             715                 720
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn
            725             730             735
Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr
        740             745             750
Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala
        755             760             765
Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly
770             775             780
Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn
785             790             795                 800
Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu
            805             810             815
Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr
        820             825             830
Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala
        835             840             845
Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu
850             855             860
His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp
865             870             875                 880
Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala
            885             890             895
Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu
        900             905             910
Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala
        915             920             925
Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr
        930             935             940
Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys
945             950             955                 960
Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile
            965             970             975
Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val
        980             985             990
Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro
        995             1000            1005
Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala
1010            1015            1020
Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp
1025            1030            1035            1040
Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser
            1045            1050            1055
Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg
            1060            1065            1070
Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp
        1075            1080            1085
Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu
        1090            1095            1100
Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn
1105            1110            1115            1120
Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro
            1125            1130            1135
Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu
        1140            1145            1150
Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu
        1155            1160            1165
```

```
Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly
    1170            1175            1180
Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
1185            1190            1195
```

<210> 32
<211> 1803
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (1)...(1803)

<223> Glyc(-)APAO coding sequence; mutation in putative
     glycosylation sites

<400> 32

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atg gca ctt gca ccg agc tac atc aat ccc cca aac gtc gcc tcc cca      48
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
 1               5               10              15

gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg      96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
                20              25              30

aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct     144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
            35              40              45

gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc     192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
     50              55              60

ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac     240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
 65              70              75              80

tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg     288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
.                85              90              95

ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg     336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
            100             105             110

cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc     384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
            115             120             125

acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg     432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
    130             135             140

gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc     480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145             150             155             160

cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta     528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
                165             170             175
```

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ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc    576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
            180                 185                 190

aac gac ctc ggc gct gcg tgg atc aat gat agc aat cag gcc gaa gta    624
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val
            195                 200                 205

tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg    672
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
            210                 215                 220

act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct    720
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225                 230                 235                 240

cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg    768
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
                245                 250                 255

gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa    816
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
            260                 265                 270

gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc    864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
            275                 280                 285

gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta    912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
            290                 295                 300

gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc    960
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305                 310                 315                 320

agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt   1008
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
                325                 330                 335

aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa   1056
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
            340                 345                 350

aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca   1104
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
            355                 360                 365

ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca   1152
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
            370                 375                 380

tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa   1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385                 390                 395                 400

aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt   1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
                405                 410                 415

tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc   1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
```

```
                    420                      425                      430

        ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg      1344
        Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
                435                      440                      445

        cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc      1392
        Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
            450                      455                      460

        tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att      1440
        Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
        465                      470                      475                  480

        acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc      1488
        Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
                        485                      490                      495

        aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac      1536
        Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
                    500                      505                      510

        gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc      1584
        Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
                515                      520                      525

        gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat      1632
        Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
                530                      535                      540

        ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc      1680
        Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
        545                      550                      555                  560

        aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg      1728
        Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
                        565                      570                      575

        tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt      1776
        Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
                        580                      585                      590

        gtg gct agc ctg gtg cca gca gca tag                                  1803
        Val Ala Ser Leu Val Pro Ala Ala  *
                    595                      600


<210> 33
<211> 600
<212> PRT
<213> Unknown

<220>
<223> Glyc(-)APAO coding sequence; mutation in putative
      glycosylation sites.

<400> 33
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
 1               5                  10                  15
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
                20                  25                  30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
```

```
                35                        40                        45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
    50                        55                        60
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65                        70                        75                        80
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
                85                        90                        95
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
                100                       105                       110
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
                115                       120                       125
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
    130                       135                       140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145                       150                       155                       160
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
                165                       170                       175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
                180                       185                       190
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val
    195                       200                       205
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
    210                       215                       220
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225                       230                       235                       240
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
                245                       250                       255
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
                260                       265                       270
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
    275                       280                       285
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
    290                       295                       300
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305                       310                       315                       320
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
                325                       330                       335
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
                340                       345                       350
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
    355                       360                       365
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
    370                       375                       380
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385                       390                       395                       400
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
                405                       410                       415
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
                420                       425                       430
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
                435                       440                       445
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
    450                       455                       460
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
465                       470                       475                       480
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
                485                       490                       495
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
    500                       505                       510
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
    515                       520                       525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
```

```
      530                      535                      540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545                      550                      555                      560
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
                565                      570                      575
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
                580                      585                      590
Val Ala Ser Leu Val Pro Ala Ala
        595                      600
```

<210> 34
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> 37-mer oligonucleotide

<400> 34
ggggaattca tggcacttgc accgagctac atcaatc                               37

<210> 35
<211> 1929
<212> DNA
<213> Exophiala spinifera

<220>
<221> intron
<222> (739)...(811)

<221> intron
<222> (1134)...(1186)

<400> 35
```
atggcacttg caccgagcta catcaatccc ccaaacgtcg cctccccagc agggtattcc      60
cacatcggcg taggcccaaa cgaagcgagg tatgtgacaa tagctggaca gattggacaa     120
gacgctttgg gcgtgacaga cccagcctac gagaaacagg ttgcccaagc attcgccaat     180
ctgcgagctt gccttgctgc agttggagcc tcttcaaacg acgtcaccaa gctcaattac     240
tacatcgtcg actacgcccc gagcaaactc accgcaattg gagatgggct gaagtctacc     300
tttgcccttg acaggctccc tccttgcacg ctggtgccag taccggcctt ggcttcacct     360
gaatacctct ttgaggttga tgccacggcg ctggtgccag acactcgac cccagacaac      420
gttgcggacg tggtagtggt gggcgctggc ttgagcggtt tggagacggc acgcaaagtc     480
caggccgccg gtctgtcctg cctcgttctt gaggcgatgg atcgtgtagg gggaaagact     540
ctgagcgtac aatcgggtcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc     600
aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcattt ggagggcgag     660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct     720
ccttatggtg actccccggt aagcacaatc ccactttgtg atgagacctc tgtcgagtgt     780
agaatacagt cactgactcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc     840
ggaactcctc cccgtatggt ctcagctgat cgaagagtat agccttgaag accccaaggc     900
gagccctcag gcgaagcggc tcgacagtgt gagcttcgcg cactactgtg agaaggacct     960
aaacttgcct gctgttctca gcgtggcaaa ccagatcaca cgcgctctgc tcggtgtgga    1020
agcccacgag atcagcatgc ttttttctcac cgactacatc aagagtgcca ccggtctcag    1080
taatattgtc tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa caggtgcgtg    1140
cggtgtcctc tcaggtaggg gactcgtttc ttagtggtca ttccaggtat gcagtcgatt    1200
tgccatgcca tgtcaaagga acttgttcca ggctcagtgc acctcaacac ccccgtcgct    1260
ggaattgagc agtcggcgtc cggctgtata gtacgatcgg cctcgggcgc cgtgttccga    1320
agcaaaaagg tggtggtttc gttaccgaca acattgtatc ccaccttgac attttcacca    1380
cctcttcccg ccgagaagca agcattggcg gaaaaatcta tcctcggcta ctatagcaag    1440
atagtcttcg tatgggacaa cccgtggtgg cgcgaacaag gcttctcggg cgtcctccaa    1500
tcgagctgtg accccatctc atttgccaga gataccagca tcgaagtcga tcggcaatgg    1560
tccattacct gtttcatggt cggagacccg ggacggaagt ggtcccaaca gtccaagcag    1620
gtacgacaaa agtctgtctg ggaccaactc cgcgcagcct acgagaacgc cggggcccaa    1680
```

```
gtcccagagc cggccaacgt gctcgaaatc gagtggtcga agcagcagta tttccaagga    1740
gctccgagcg ccgtctatgg gctgaacgat ctcatcacac tgggttcggc gctcagaacg    1800
ccgttcaagt gtgttcattt cgttggaacg gagacgtctt tagtttggaa agggtatatg    1860
gaaggggcca tacgatcggg tcaacgaggt gctgcagaag ttgtggctag cctggtgcca    1920
gcagcatag                                                            1929
```

<210> 36
<211> 600
<212> PRT
<213> Exophiala spinifera

<400> 36

```
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1               5                   10                  15
Ala Gly Tyr Ser His Ile Gly Val Gly Pro Asn Glu Ala Arg Tyr Val
                20                  25                  30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro
        35                  40                  45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
    50                  55                  60
Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr
65                  70                  75                  80
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
                85                  90                  95
Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
            100                 105                 110
Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
            115                 120                 125
Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
        130                 135                 140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145                 150                 155                 160
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
                165                 170                 175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
            180                 185                 190
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
            195                 200                 205
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
    210                 215                 220
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225                 230                 235                 240
Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
                245                 250                 255
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu
            260                 265                 270
Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
    275                 280                 285
Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val
    290                 295                 300
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305                 310                 315                 320
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
            325                 330                 335
Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
            340                 345                 350
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
        355                 360                 365
Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
370                 375                 380
Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385                 390                 395                 400
```

```
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
            405             410             415
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
            420             425             430
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp
            435             440             445
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
    450             455             460
Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile
465             470             475             480
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
            485             490             495
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
            500             505             510
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
            515             520             525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
            530             535             540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545             550             555             560
Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
            565             570             575
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
            580             585             590
Val Ala Ser Leu Val Pro Ala Ala
            595             600
```

<210> 37
<211> 1929
<212> DNA
<213> Exophiala spinifera

<220>
<221> intron
<222> (739)...(811)

<221> intron
<222> (1134)...(1186)

<400> 37
```
atggcacttg caccgagcta catcaatccc ccaaacgtcg cctccccagc agggtattcc    60
cacatcggcg taggcccaaa cgaagcgagg tatgtgacaa tagctggaca gattggacaa   120
gacgctttgg gcgtgacaga cccagcctac gagaaacagg ttgcccaagc attcgccaat   180
ctgcgagctt gccttgctgc agttggagcc tcttcaaacg acgtcaccaa gctcaattac   240
tacatcgtcg actacgcccc gagcaaactc accgcaattg agatgggct gaagtctacc    300
tttgcccttg acaggctccc tccttgcacg ctggtgccag taccggcctt ggcttcacct   360
gaatacctct ttgaggttga cgccacggcg ctggtgccag acactcgac cccagacaac    420
gttgcggacg tggtagtggt gggcgctggc ttgagcggct ggagacggc acgcaaagtc    480
caggccgccg gtctgtcctg cctcgttctt gaggcgatgg atcgtgtagg gggaaagact   540
ctgagcgtac aatcgggtcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc    600
aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcattt ggagggcgag   660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct   720
ccttatggtg actccccggt aagcacaatc ccactttgtg atgagacctc tgtcgagtgt   780
agaatacagt cactgactcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc    840
ggaactcctc cccgtatggt ctcagctgat cgaagagtat agccttgaag accccaaggc   900
gagccctcag gcgaagcggc tcgacagtgt gagcttcgcg cactactgtg agaaggacct   960
aaacttgcct gctgttctca gcgtggcaaa ccagatcaca cgcgctctgc tcggtgtgga  1020
agcccacgag atcagcatgc tttttctcac cgactacatc aagagtgcca ccggtctcag  1080
taatattgtc tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa caggtgcgtg  1140
cggtgtcctc tcaggtaggg gactcgtttc ttagtggtca ttccaggtat gcagtcgatt  1200
tgccatgcca tgtcaaagga acttgttcca ggctcagtgc acctcaacac ccccgtcgct  1260
ggaattgagc agtcggcgtc cggctgtata gtacgatcgg cctcgggcgc cgtgttccga  1320
```

```
agcaaaaagg tggtggtttc gttaccgaca acattgtatc ccaccttgac attttcacca    1380
cctcttcccg ccgagaagca agcattggcg gaaaaatcta tcctcggcta ctatagcaag    1440
atagtcttcg tatgggacaa cccgtggtgg cgcgaacaag gcttctcggg cgtcctccaa    1500
tcgagctgtg accccatctc atttgccaga gataccagca tcgaagtcga tcggcaatgg    1560
tccattacct gtttcatggt cggagacccg ggacggaagt ggtcccaaca gtccaagcag    1620
gtacgacaaa agtctgtctg gaccaactc cgcgcagcct acgagaacgc cggggcccaa    1680
gtcccagagc cggccaacgt gctcgaaatc gagtggtcga agcagcagta tttccaagga    1740
gctccgagcg ccgtctatgg gctgaacgat ctcatcacac tgggttcggc gctcagaacg    1800
ccgttcaagt gtgttcattt cgttggaacg gagacgtctt tagtttggaa agggtatatg    1860
gaaggggcca tacgatcggg tcaacgaggt gctgcagaag ttgtggctag cctggtgcca    1920
gcagcatag                                                            1929
```

`<210>` 38
`<211>` 600
`<212>` PRT
`<213>` Exophiala spinifera

`<400>` 38

```
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1               5                   10                  15
Ala Gly Tyr Ser His Ile Gly Val Gly Pro Asn Glu Ala Arg Tyr Val
            20                  25                  30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro
        35                  40                  45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
    50                  55                  60
Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr
65                  70                  75                  80
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
                85                  90                  95
Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
            100                 105                 110
Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
        115                 120                 125
Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
        130                 135                 140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145                 150                 155                 160
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
                165                 170                 175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
            180                 185                 190
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
        195                 200                 205
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
210                 215                 220
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225                 230                 235                 240
Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
                245                 250                 255
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu
            260                 265                 270
Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
        275                 280                 285
Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val
    290                 295                 300
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305                 310                 315                 320
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
                325                 330                 335
Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
            340                 345                 350
```

```
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
        355                 360             365
Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
        370                 375             380
Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385                 390                 395                 400
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
                405                 410                 415
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
                420                 425             430
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp
        435                 440                 445
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
        450                 455             460
Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile
465                 470                 475                 480
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
                485                 490                 495
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
                500                 505             510
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
        515                 520             525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
        530                 535             540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545                 550                 555                 560
Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
                565                 570                 575
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
        580                 585             590
Val Ala Ser Leu Val Pro Ala Ala
        595                 600
```

```
<210> 39
<211> 1930
<212> DNA
<213> Exophiala spinifera

<220>
<221> intron
<222> (739)...(811)

<221> intron
<222> (1134)...(1187)

<221> misc_feature
<222> (648)...(648)
<223> n = A,T,C or G

<400> 39
atggcacttg caccgagcta catcaatccc ccaaacgtcg cctccccagc agggtattct    60
cacgtcggcg taggcccaga cggagggagg tatgtgacaa tagctggaca gattggacaa   120
gacgcttcgg gcgtgacaga ccctgcctac gagaaacagg ttgcccaagc attcgccaat   180
ctgcgagctt gccttgctgc agttggagcc acttcaaacg acgtcaccaa gctcaattac   240
tacatcgtcg actacgcccc gagcaaactc accgcaattg agatgggct gaaggctacc    300
tttgcccttg acaggctccc tccttgcacg ctggtgccag tgtcggcctt gtcttcacct   360
gaatacctct ttgaggttga tgccacggcg ctggtgccgg acacacgac cccagacaac    420
gttgcggacg tggtagtggt gggcgctggc ttgagcggtt ggagacggc acgcaaagtc    480
caggccgccg tctgtcctg cctcgttctt gaggcgatgg atcgtgtagg gggaaagact    540
ctgagcgtac aatcgggtcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc    600
aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcatnt ggagggcgag    660
ctccagagga cgactggaaa ttcaatccat caagcacaag acggtacaac cactacagct    720
```

```
ccttatggtg actccttggt aagcacaatc ccactttgtg atgagacctc tgtcgagtgt    780
agaatacagt cactgattcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc    840
ggaactcctc cccgtatggt ctcagctgat cgaagagcat agccttcaag acctcaaggc    900
gagccctcag gcgaagcggc tcgacagtgt gagcttcgcg cactactgtg agaaggaact    960
aaacttgcct gctgttctcg gcgtagcaaa ccagatcaca cgcgctctgc tcggtgtgga   1020
agcccacgag atcagcatgc tttttctcac cgactacatc aagagtgcca ccggtctcag   1080
taatattttc tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa caggtgcgtg   1140
tggtgtcgtc tcaggtgggg gactcgtttc tcaagtggtc atttcaggta tgcagtcgat   1200
ttgccatgcc atgtcaaagg aacttgttcc aggctcagtg cacctcaaca ccccgtcgc    1260
tgaaattgag cagtcggcat ccggctgtac agtacgatcg gcctcgggcg ccgtgttccg   1320
aagcaaaaag gtggtggttt cgttaccgac aaccttgtat cccaccttga cattttcacc   1380
acctctcccc gccgagaagc aagcattggc ggaaaattct atcctgggct actatagcaa   1440
gatagtcttc gtatgggaca agccgtggtg gcgcgaacaa ggcttctcgg cgtcctcca    1500
atcgagctgt gaccccatct catttgccag agataccagc atcgacgtcg atcgacaatg   1560
gtccattacc tgtttcatgg tcggagaccc gggacggaag tggtcccaac agtccaagca   1620
ggtacgacaa aagtctgtct gggaccaact ccgcgcagcc tacgagaacg ccggggccca   1680
agtcccagag ccggccaacg tgctcgaaat cgagtggtcg aagcagcagt atttccaagg   1740
agctccgagc gccgtctatg ggctgaacga tctcatcaca ctgggttcgg cgctcagaac   1800
gccgttcaag agtgttcatt tcgttggaac ggagacgtct ttagtttgga aagggtatat   1860
ggaaggggcc atacgatcgg gtcaacgagg tgctgcagaa gttgtggcta gcctggtgcc   1920
agcagcatag                                                          1930
```

<210> 40
<211> 598
<212> PRT
<213> Exophiala spinifera

<220>
<221> VARIANT
<222> (216)...(216)
<223> Xaa = Any Amino Acid

<400> 40
```
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1               5                   10                  15
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
            20                  25                  30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
        35                  40                  45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
    50                  55                  60
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65                  70                  75                  80
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
            85                  90                  95
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
            100                 105                 110
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
            115                 120                 125
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
            130                 135                 140
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
145                 150                 155                 160
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
                165                 170                 175
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
            180                 185                 190
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
            195                 200                 205
Arg Leu Phe Glu Arg Phe His Xaa Glu Gly Glu Leu Gln Arg Thr Thr
210                 215                 220
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
```

```
225                    230                    235                    240
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
                245                    250                    255
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp
                260                    265                    270
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala
                275                    280                    285
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Asn
                290                    295                    300
Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met
305                    310                    315                    320
Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile
                325                    330                    335
Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly
                340                    345                    350
Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser
                355                    360                    365
Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly
                370                    375                    380
Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val
385                    390                    395                    400
Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro
                405                    410                    415
Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly
                420                    425                    430
Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu
                435                    440                    445
Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe
                450                    455                    460
Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys
465                    470                    475                    480
Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln
                485                    490                    495
Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn
                500                    505                    510
Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp
                515                    520                    525
Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu
                530                    535                    540
Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser
545                    550                    555                    560
Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met
                565                    570                    575
Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala
                580                    585                    590
Ser Leu Val Pro Ala Ala
                595
```

<210> 41
<211> 1928
<212> DNA
<213> Rhinocladiella atrovirens

<220>
<221> intron
<222> (739)...(811)

<221> intron
<222> (1134)...(1185)

<400> 41
atggcacttg caccgagcta catcaatccc ccaaacctcg cctccccagc agggtattcc      60

```
                  180                       185                       190
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
          195                       200                       205
Phe Lys Leu Phe Glu Arg Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
    210                       215                       220
Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr
225                       230                       235                       240
Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu
              245                       250                       255
Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro
          260                       265                       270
Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His
    275                       280                       285
Tyr Cys Glu Lys Asp Leu Ser Leu Pro Ala Val Leu Gly Val Ala Asn
    290                       295                       300
Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met
305                       310                       315                       320
Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile
              325                       330                       335
Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly
              340                       345                       350
Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser
          355                       360                       365
Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly
    370                       375                       380
Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val
385                       390                       395                       400
Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro
              405                       410                       415
Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Leu Gly
              420                       425                       430
Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu
          435                       440                       445
Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe
    450                       455                       460
Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile Thr Cys
465                       470                       475                       480
Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln
              485                       490                       495
Val Arg Gln Lys Ser Val Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn
          500                       505                       510
Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp
          515                       520                       525
Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Val Val Tyr Gly Leu
    530                       535                       540
Asn Cys Leu Asn Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Gly
545                       550                       555                       560
Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met
              565                       570                       575
Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala
          580                       585                       590
Ser Leu Val Pro Ala Ala
          595
```

<221> intron
<222> (1134)...(1186)

<400> 43
```
atggcacttg caccgagcta catcaatccc ccaaacctcg cctccccagc agggtattcc        60
tacgtcggcg taggcccaaa cggaggagg tatgtgacaa tagctggaca gattggacaa       120
gacgcttcgg ccgtgacaga ccctgcctac gagaaacagg ttgcccaagc attcgccaac      180
ctgcgagctt gtcttgctgc agttggagcc acttcaaacg acattaccaa gctcaattac      240
tacatcgtcg actacaaccc gagcaaactc accgcaattg gagatgggct gaaggctacc      300
tttgcccttg acaggctccc tccttgcacg ctggtgccag tgccggccct ggcttcacct      360
gaatacctct ttgaggttga tgccacggcg ctggttccag gacactcaac cccagacaat      420
gttgcggacg tggtcgtggt gggcgctggc ttgagcggtt tggagacggc acgcaaagtc      480
caggctgccg ggctgtcctg cctcgttctt gaggcgatgg atcgtgtggg gggaaagact      540
ctgagcgtac aatcgggtcc cggcaggacg actatcaatg acctcggcgc tgcgtggatc      600
aatgacagca accaaagcga agtattcaaa ttatttgaaa gatttcattt ggagggcgag      660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct      720
ccttatggtg attccctggt aagcacaatt ccatcttgtg atgagacctc tgtcgtgtgt      780
agaatacagt cgctgactcc acatcgtcca gctgagcgag gaggttgcaa gtgcactcgc      840
ggaactcctt cccgcatggt ctcagctgat cgaagagcat agtcttgaag accccaaggc      900
gagccctcaa gcgaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct      960
aaacttgcct gctgttctcg gcgtggcaaa ccagatcaca cgcgctctgc tcggtgtgga     1020
agcccacgag atcagcatgt tttttctcac cgactacatc aagagtgcca ccggtctcag     1080
taatattgtc tcggataaga aagacggtgg gcagtatatg cgatgcaaaa caggtgcgtg     1140
tggtgttctc tcagtgggag actcgtttct tagtggtcat tccaggtatg cagtcgcttt     1200
gccatgccat gtcaaaggaa cttgttccag gctcagtgca cctcaacacc ccgtcgccg      1260
aaattgagca gtcggcatcc ggctgtacag tacgatcggc ctcgggcggc gtgttccgaa     1320
gtaaaaaggt ggtggtttcg ttaccgacaa ccttgtatcc caccttgata tttcaccac      1380
ctcttcccgc cgagaagcaa gcattggctg aaaaatccat cctgggctac tatagcaaga     1440
tagtcttcgt atgggacaag ccgtggtggc gcgaacaagg cttctcgggc gtcctccaat     1500
cgagctgtga ccccatctca tttgccagag ataccagcat cgaagtcgat cggcaatggt     1560
ccattacctg tttcatggtc ggagacccgg gacggaagtg gtcccaacag tccaagcagg     1620
tacgacagaa gtctgtctgg aaccaactcc gcgcagccta cgagaacgcc ggggcccaag     1680
tcccagagcc ggccaacgtg ctcgagatcg agtggtcgaa gcagcagtat ttccaaggag     1740
cgccgagcgc cgtctatggg ctgaactgtc tcaacacact gggttcggcg ctcagaacgc     1800
cgttcaaggg tgttcatttc gttggaacgg agacgtcttt ggtttggaaa gggtatatgg     1860
aagggccat acgatcgggt cagcgaggcg ctgcagaagt tgtggctagc ctggtgccag     1920
cagcatag                                                               1928
```

<210> 44
<211> 591
<212> PRT
<213> Rhinocladiella atrovirens

<400> 44
```
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Leu Ala Ser Pro
1               5                   10                  15
Ala Gly Tyr Ser Tyr Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val
                20                  25                  30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro
        35                  40                  45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
        50                  55                  60
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
65                  70                  75                  80
Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
                85                  90                  95
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
                100                 105                 110
Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
        115                 120                 125
Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
```

```
          130                     135                     140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145                     150                     155                     160
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
                165                     170                     175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Gly Arg Thr Thr Ile Asn
            180                     185                     190
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Lys
        195                     200                     205
Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
    210                     215                     220
Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr
225                     230                     235                     240
Gly Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu
                245                     250                     255
Pro Ala Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro Lys Ala
                260                     265                     270
Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His Tyr Cys
            275                     280                     285
Glu Lys Leu Asn Leu Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg
            290                     295                     300
Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Phe Phe Leu Thr
305                     310                     315                     320
Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Val Ser Asp Lys
                325                     330                     335
Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Leu
            340                     345                     350
Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn
            355                     360                     365
Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg
            370                     375                     380
Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val Val Leu Pro Thr
385                     390                     395                     400
Leu Tyr Pro Thr Leu Ile Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
                405                     410                     415
Ala Leu Ala Glu Lys Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
                420                     425                     430
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
            435                     440                     445
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Glu
            450                     455                     460
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
465                     470                     475                     480
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
                485                     490                     495
Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
            500                     505                     510
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
            515                     520                     525
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly
            530                     535                     540
Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu
545                     550                     555                     560
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
                565                     570                     575
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
            580                     585                     590
```

<220>
<221> intron
<222> (739)...(811)

<221> intron
<222> (1134)...(1185)

<400> 45
```
atggcacttg caccgagcta catcaatccc ccaaacctcg cctccccagc agggtattcc    60
cacgtcggcg taggcccaaa cggagggagg tatgtgacaa tagctggaca gattggacaa   120
gacgcttcgg ccgtgacaga ccctgcctac gagaaacagg ttgcccaagc attcgccaac   180
ctgcgagctt gtcttgctgc agttggagcc acttcaaacg acattaccaa gctcaattac   240
tacatcgtcg actacaaccc gagcaaactc accgcaattg gagatgggct gaaggctacc   300
tttgcccttg acaggctccc tccttgcacg ctggtgccag tgccggccct ggcttcacct   360
gaatacctct ttgaggttga tgctacggcg ctggttccag acactcaac cccagacaat   420
gttgcggacg tggtcgtggt gggcgctggc ttgagcggtt tggagacggc acgcaaagtc   480
caggctgccg ggctgtcctg cctcgttctt gaggcgatgg atcgtgtggg gggaaagact   540
ctgagcgtac aatcgggtcc cggcaggacg actatcaatg acctcggcgc tgcgtggatc   600
aatgacagca accaaagcga agtattcaaa ttatttgaaa gatttcattt ggagggcgag   660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct   720
ccttatggtg attccctggt aggcacaatt ccatcttgtg atgagacctc tgtcgtgtgt   780
agaatacagt cgctgactcc acatcgtcca gctgagcgag gaggttgcaa gtgcactcgc   840
ggaactcctt cccgcatggt ctcagctgat cgaagagcat agtcttgaag accccaaggc   900
gagccctcaa gcgaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct   960
aaacttgcct gctgttctcg gcgtggcaaa ccagatcaca cgcgctctgc tcggtgtgga  1020
agcccacgag atcagcatgc tttttctcac cgactacatc aagagtgcca ccggtctcag  1080
taatattgtc tcggataaga aagacggtgg gcagtatatg cgatgcaaaa caggtgcgtg  1140
tggtgttctc tcagtgggag actcgtttct tagtggtcat ccaggtatg cagtcgcttt   1200
gccatgccat gtcaaaggaa cttgttccag gctcagtgca cctcaacacc ccgtcgccg   1260
aaattgagca gtcggcatcc ggctgtacag tacgatcggc ctcgggcggc gtgttccgaa  1320
gtaaaaaggt ggtggtttcg ttaccgacaa ccttgtatcc caccttgata ttttcaccac  1380
ctcttcccgc cgagaagcaa gcattggctg aaaaatccat cctgggctac tatagcaaga  1440
tagtcttcgt atgggacaag ctgtggtggc gcgaacaagg cttctcgggc gtcctccaat  1500
cgagctgtga ccccatctca tttgccagag ataccagcat cgaagtcgat cggcaatggt  1560
ccattacctg tttcatggtc ggagacccgg acggaagtg gtcccaacag tccaagcagg  1620
tacgacagaa gtctgtctgg aaccaactcc gcgcagccta cgagaacgcc ggggcccaag  1680
tcccagagcc ggccaacgtg ctcgagatcg agtggtcgaa gcagcagtat ttccaaggag  1740
cgccgagcgc cgtctatggg ctgaactgtc tcaacacact gggttcggcg ctcagaacgc  1800
cgttcaaggg tgttcatttc gttggaacgg agacgtcttt ggtttggaaa gggtatatgg  1860
aaggggccat acgatcgggt cagcgaggcg ctgcagaagt tgtgcctagc ctggtgccag  1920
cagcatag                                                           1928
```

<210> 46
<211> 591
<212> PRT
<213> Rhinocladiella atrovirens

<400> 46
```
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Ala Ser Pro Ala
1               5                  10                  15
Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val Thr
            20                  25                  30
Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro Ala
        35                  40                  45
Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu
    50                  55                  60
Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr Tyr
65                  70                  75                  80
Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly Leu
                85                  90                  95
Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val Pro
```

```
                    100                      105                      110
Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala Thr
        115                      120                      125
Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val Val
        130                      135                      140
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
145                      150                      155                      160
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
                165                      170                      175
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
                180                      185                      190
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Phe
        195                      200                      205
Lys Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
        210                      215                      220
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
225                      230                      235                      240
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
                245                      250                      255
Leu Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp
                260                      265                      270
Pro Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala
        275                      280                      285
His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Gly Val Ala
        290                      295                      300
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
305                      310                      315                      320
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
                325                      330                      335
Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr
                340                      345                      350
Gly Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
        355                      360                      365
Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
        370                      375                      380
Gly Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys
385                      390                      395                      400
Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro Leu
                405                      410                      415
Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Gly Tyr Tyr Ser
                420                      425                      430
Lys Ile Val Phe Val Asp Lys Leu Trp Trp Arg Glu Gln Gly Phe Ser
        435                      440                      445
Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr
        450                      455                      460
Ser Ile Glu Val Asp Arg Gln Ser Ile Thr Cys Phe Met Val Gly Asp
465                      470                      475                      480
Pro Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val
                485                      490                      495
Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro
                500                      505                      510
Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe
        515                      520                      525
Gln Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly
        530                      535                      540
Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu
545                      550                      555                      560
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
                565                      570                      575
Gln Arg Gly Ala Ala Glu Val Val Pro Ser Leu Val Pro Ala Ala
        580                      585                      590
```

<210> 47
<211> 600
<212> PRT
<213> Exophiala spinifera

<400> 47
```
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
 1               5                  10                  15
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
            20                  25                  30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
        35                  40                  45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
    50                  55                  60
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65                  70                  75                  80
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
                85                  90                  95
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
            100                 105                 110
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
            115                 120                 125
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
    130                 135                 140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145                 150                 155                 160
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
                165                 170                 175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
            180                 185                 190
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
            195                 200                 205
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
    210                 215                 220
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225                 230                 235                 240
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
                245                 250                 255
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
            260                 265                 270
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
    275                 280                 285
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
    290                 295                 300
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305                 310                 315                 320
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
                325                 330                 335
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
            340                 345                 350
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
    355                 360                 365
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
    370                 375                 380
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385                 390                 395                 400
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
                405                 410                 415
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
            420                 425                 430
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
            435                 440                 445
```

```
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
    450             455             460
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
465             470             475             480
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
            485             490             495
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
        500             505             510
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
    515             520             525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
    530             535             540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545             550             555             560
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
            565             570             575
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
        580             585             590
Val Ala Ser Leu Val Pro Ala Ala
        595             600
```

<210> 48
<211> 1392
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteine 461

<400> 48
```
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt        48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1               5               10              15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt        96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
            20              25              30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg       144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
        35              40              45

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat       192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
    50              55              60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg       240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65              70              75              80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa       288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
            85              90              95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag       336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
        100             105             110

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg       384
```

```
        Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
                115                 120                 125

atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag          432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
    130                 135                 140

cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac          480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145                 150                 155                 160

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc          528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
                165                 170                 175

ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc          576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
                180                 185                 190

aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc          624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
                195                 200                 205

ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc          672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
    210                 215                 220

atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc          720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225                 230                 235                 240

gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg          768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
                245                 250                 255

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc          816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
                260                 265                 270

ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa          864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
                275                 280                 285

gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc          912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
    290                 295                 300

gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc          960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305                 310                 315                 320

caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac         1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
                325                 330                 335

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga         1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
                340                 345                 350

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg         1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
                355                 360                 365
```

```
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag        1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
    370                 375                 380

ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa        1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385                 390                 395                 400

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt        1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
                405                 410                 415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag        1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
            420                 425                 430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt        1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
            435                 440                 445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag        1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  *
    450                 455                 460
```

<210> 49
<211> 463
<212> PRT
<213> Unknown

<220>
<223> Cys (-) APAO; removal of cysteine 461

<400> 49
```
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1               5                   10                  15
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
            20                  25                  30
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
            35                  40                  45
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
        50                  55                  60
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65                  70                  75                  80
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
            85                  90                  95
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
            100                 105                 110
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
            115                 120                 125
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
            130                 135                 140
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145                 150                 155                 160
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
                165                 170                 175
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
            180                 185                 190
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
        195                 200                 205
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
```

```
            210                  215                  220
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225                  230                  235                  240
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
                    245                  250                  255
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
            260                  265                  270
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
            275                  280                  285
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
            290                  295                  300
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305                  310                  315                  320
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
                    325                  330                  335
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
            340                  345                  350
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
            355                  360                  365
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
            370                  375                  380
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385                  390                  395                  400
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
            405                  410                  415
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
            420                  425                  430
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
            435                  440                  445
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
            450                  455                  460
```

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<210> 50
<211> 1392
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 50
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt     48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1               5                   10                  15


ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt    96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
                20                  25                  30


ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg   144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
            35                  40                  45


ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat   192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
     50                  55                  60


gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg   240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
```

```
         65                      70                      75                      80
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa        288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
                    85                  90                  95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag        336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
                100                 105                 110

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg        384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
                115                 120                 125

atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag        432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
        130                 135                 140

cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac        480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145                 150                 155                 160

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc        528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
                165                 170                 175

ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc        576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
                180                 185                 190

aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc        624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
                195                 200                 205

ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc        672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala
        210                 215                 220

atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc        720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225                 230                 235                 240

gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg        768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
                245                 250                 255

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc        816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
                260                 265                 270

ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa        864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
                275                 280                 285

gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc        912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
        290                 295                 300

gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc        960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305                 310                 315                 320
```

```
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac       1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
                325             330             335

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga       1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
                340             345             350

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg       1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
                355             360             365

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag       1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
                370             375             380

ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa       1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385             390             395             400

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt       1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
                405             410             415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag       1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
                420             425             430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt       1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
                435             440             445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag       1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  *
                450             455             460
```

<210> 51
<211> 463
<212> PRT
<213> Unknown

<220>
<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 51
```
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
  1               5                   10                  15
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
              20                  25                  30
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
              35                  40                  45
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
          50                  55                  60
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65                  70                  75                  80
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
                  85                  90                  95
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
              100                 105                 110
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
              115                 120                 125
```

```
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
    130             135             140
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145             150             155             160
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
            165             170             175
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
            180             185             190
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
            195             200             205
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala
    210             215             220
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225             230             235             240
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
            245             250             255
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
            260             265             270
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
    275             280             285
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
    290             295             300
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305             310             315             320
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
            325             330             335
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
            340             345             350
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
            355             360             365
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
    370             375             380
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385             390             395             400
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
            405             410             415
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
            420             425             430
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
            435             440             445
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
    450             455             460
```

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<210> 52
<211> 1392
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteines 169, 359, and
      461

<400> 52
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt    48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1               5                  10                  15


ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg agc tcc ctc gtt    96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val
```

```
                  20                        25                        30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg        144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
        35                      40                      45

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat        192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
        50                      55                      60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg        240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65                      70                      75                      80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa        288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
                85                      90                      95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag        336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
                100                     105                     110

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg        384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
                115                     120                     125

atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag        432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
        130                     135                     140

cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac        480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145                     150                     155                     160

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc        528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
                165                     170                     175

ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc        576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
                180                     185                     190

aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc        624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
                195                     200                     205

ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc        672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala
        210                     215                     220

atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc        720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225                     230                     235                     240

gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg        768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
                245                     250                     255

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc        816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
        260                     265                     270
```

```
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa        864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
        275                 280                 285

gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc        912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
        290                 295                 300

gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc        960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305                 310                 315                 320

caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac       1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
                325                 330                 335

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga       1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
                340                 345                 350

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg       1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
        355                 360                 365

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag       1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
        370                 375                 380

ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa       1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385                 390                 395                 400

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt       1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
                405                 410                 415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag       1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
        420                 425                 430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt       1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
        435                 440                 445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag       1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *
        450                 455                 460
```

<210> 53
<211> 463
<212> PRT
<213> Unknown

<220>
<223> Cys (-) APAO; removal of cysteines 169, 359, and
      461

<400> 53
```
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1               5                   10                  15
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val
```

```
                    20                      25                      30
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
        35                      40                      45
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
        50                      55                      60
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65                      70                      75                      80
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
                85                      90                      95
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
            100                     105                     110
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
        115                     120                     125
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
    130                     135                     140
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145                     150                     155                     160
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
                165                     170                     175
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
            180                     185                     190
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
        195                     200                     205
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala
    210                     215                     220
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225                     230                     235                     240
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
                245                     250                     255
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
            260                     265                     270
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
        275                     280                     285
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
    290                     295                     300
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305                     310                     315                     320
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
                325                     330                     335
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
            340                     345                     350
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
        355                     360                     365
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
    370                     375                     380
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385                     390                     395                     400
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
                405                     410                     415
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
        420                     425                     430
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
        435                     440                     445
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
    450                     455                     460
```

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